

genome

AGATACAGCCATGACCGTAGCATGCTAACTGTGACGGGCATTAC

reads

TGACCGTAGCATGCT ①
GACCGTAGCATGCTA ②

TGACCG ①
GACCGT ① ②

extract the read's
 k -mers ($k=6$)

TAGCAT ① ②
AGCATG ① ②
GCATGC ① ②
CATGCT ① ②
ATGCTA ②

TGACCGTAGCATGCTA
a sequence from the genome